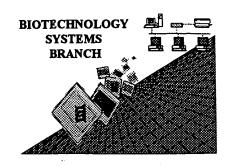
Ternan

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 19/29, 565

Art Unit / Team No.: 1643

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

	ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09//29/36	>
ATTI	N: NEW RULES CASES: I Wrapped Nudelcs	PLEASE DISREGARD ENGLISH "ALPHA" HE The number/text at the end of each line "wrap This may occur if your file was retrieved in a v Please adjust your right margin to .3, as this	vord processor after creating it.	₹E
2	_ Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".		
3	_ Incorrect Line Length	The rules require that a line not exceed 72 changes and the rules require that a line not exceed 72 changes.	aracters in length. This includes spaces.	
4	_ Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.		•
5 <u>V</u>	_ Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.		-
6	Variable Length	Sequence(s) contain n's or Xaa's which is As per the rules, each n or Xaa can only repre Please present the maximum number of each Indicate in the (ix) features section that some	sent a single residue. residue having variable length and	
7	Wrong Designation	Sequence(s) contain amino acid or nucle representations as per the Sequence Rules (P	ic acid designators which are not standard lease refer to paragraph 1.822)	
8	Skipped Sequences (OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:	se use the following format for each skipped sequence: Insert any headings under "SEQUENCE CHARACTERIS K:	TICS")
		Please also adjust the "(iii) NUMBER OF SEQ	UENCES:" response to include the skipped sequence(s).	
9	Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, pleas <210> sequence Id number <400> sequence Id number 000	e use the following format for each skipped sequence.	
)	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in Use of <220> to <223> is MANDATORY if n's of (220> to <223> section, please explain local	the Sequence Listing. or Xaa's are present. tion of n or Xaa, and which residue n or Xaa represents.	
·	Use of <213>Organism (NEW RULES)	Sequence(s) are missing this mandat	ory field or its response.	
!	Use of <220>Feature (NEW RULES)	Sequence(s) are missing the <220>Feature Use of <220> to <223> is MANDATORY if <21; Please explain source of genetic material in (See "Federal Register," 6/01/98, Vol. (Sec. 1.823 of new Sequence Rules)	3>ORGANISM Is "Artificial" or "Unknown" <220> to <223> section.	
	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function o	f Patentin version 2.0. This causes a corrupted nititiers and responses (as indicated on raw sequence list means to copy file to floopy disk.	ing).

lese MANDATTER ruenew idestripen ord their response are shown at the beginning 09/129565 SEQUENCE LISTING

Vegested) These MANDATELY rusnew idestrying L 1207 L1367 Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ilé

1 5 10 15 thean ersure arred and Ile Leu Met Cys Phe Ser Ile Asp Ser Pro There humber are aligned mardetay properly. DO NOT use TAB humeric. codes between overd and , der Lifieri puroper. Use space characters. and responsed are show in his file is enable, per new sequence lock sequere Rebe, It is mening mandatory numeric identifiers and their regionse see sample Sequence Listing (attacked) for valid format. also, correlt seu segvere Ruler for guidone. Plese see Den 5 om Enn Surmay Sleet very important allakrown," Hylan' in 22207-12237 seetin (1) please somme to page too oppen en'

Appendix A To Subpart G to Part 1-Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

<130> 01-00001

<140> US 08/999,999

<141> 1998-02-28

<150> EP 91000000

<151> 1997-12-31

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<3.05> 4

<3.06> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatett ctttggatet ctgagtetge ctgagtggta 60

ctcttgagte ctggagatet ctcctcteae atgtgategt cgagactgae cgatagateg 120

ctgactgact ctgagatagt cgagecegta cgagacegt cgagggtgae agagagtggg 180

cgegtgegeg cagagegeg cgeeggtgeg cgegegagtg cgeggtggge cgegegaggg 240

ctttegegge ageggeggeg cttteeggeg cgegecegte cgeecetaga cetgagaggt 300

cttetettee cteetettea ctagagaggt ctatatatac atg gtt tea atg ttc 355

Met Val Ser Met Phe

E

age ttg tet tte aaa tgg eet gga ttt tgt ttg ttt gtt tgtttgete

403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

· 10

15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

ales and Regulations

Phe Val

ed: May 22, 1998.

A. Lehman,
ant Secretary of Commerce and
alssioner of Patents and Trademarks.
oc. 98-14194 Filed 5-29-98; 8:45 am]
CODE 3510-16-C